IN THE SPECIFICATION

Please replace the paragraph beginning at page15, line 5, with the following amended paragraph:

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at ~~http://www.~~ncbi.nlm.nih.gov/BLAST/. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at ~~http://www.~~ncbi.nlm.nih.gov/gorf/bl2.html. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Please replace the paragraph beginning at page 53, line 23, with the following amended paragraph:

Transcript images which profile the expression of the polynucleotides of the present invention may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known

toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at ~~http://www.~~niehs.nih.gov/oc/news/toxchip.htm.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

Please amend the first and second columns of Table 1, beginning at page 72, as follows:

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:
1	12
2	13
3	14
4	15
5	16
6	17
~~7~~ 11	~~18~~ 22
~~8~~ 7	~~19~~ 18
~~9~~ 8	~~20~~ 19
~~10~~ 9	~~21~~ 20
~~11~~ 10	~~22~~ 21

Please amend the first column of Table 2, beginning at page 73, as follows:

Seq ID NO:
1
2
3
4
5
6
~~7~~ 11
~~8~~ 7
~~9~~ 8
~~10~~ 9
~~11~~ 10

Please amend the first column of Table 3, beginning at page 76, as follows:

Nucleotide SEQ ID NO:
12
13
14
15
16
17
~~18~~ 22
~~19~~ 18
~~20~~ 19
~~21~~ 20
~~22~~ 21

Please amend the first column of Table 4, beginning at page 77, as follows:

Nucleotide SEQ ID NO:
12
13
14
15
16
17
~~18~~ 22
~~19~~ 18
~~20~~ 19
~~21~~ 20
~~22~~ 21